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RAW SEQUENCE LISTING DATE: 05/16/2002
PATENT APPLICATION: US/10/083,825 TIME: 14:14:06

Input Set : N:\Crf3\RULE60\10083825.raw
Output Set: N:\CRF3\05162002\J083825.raw

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: KHOURI, ROGER K.
SAMPATH, KUBER T.
RUEGER, DAVID C.

(ii) TITLE OF INVENTION: MANUFACTURE OF AUTOGENOUS REPLACEMENT BODY PARTS

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: TESTA, HURWITZ & THIBEAULT
(B) STREET: 53 STATE STREET
(C) CITY: BOSTON
(D) STATE: MASSACHUSETTS
(E) COUNTRY: U.S.A.
(F) ZIP: 02109

ENTERED

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
C--> **(A) APPLICATION NUMBER: US/10/083,825**
C--> **(B) FILING DATE: 27-Feb-2002**
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/459,129
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: KELLEY, ROBIN D.
(B) REGISTRATION NUMBER: 34,637
(C) REFERENCE/DOCKET NUMBER: CRP-101

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 617/248-7000
(B) TELEFAX: 617/248-7100

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1822 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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```
61     (vi) ORIGINAL SOURCE:
62          (A) ORGANISM: HOMO SAPIENS
63          (F) TISSUE TYPE: HIPPOCAMPUS
65     (ix) FEATURE:
66          (A) NAME/KEY: CDS
67          (B) LOCATION: 49..1341
68          (C) IDENTIFICATION METHOD: experimental
69          (D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
70 /product= "OP1"
71 /evidence= EXPERIMENTAL
72 /standard_name= "OP1"
75     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
77 GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG       57
78                                                      Met His Val
79                                                        1
81 CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA       105
82 Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
83       5                  10                  15
85 CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC       153
86 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
87  20                  25                  30                  35
89 GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG       201
90 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
91                  40                  45                  50
93 CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC       249
94 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
95              55                  60                  65
97 CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG       297
98 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
99          70                  75                  80
101 CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC       345
102 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
103      85                  90                  95
105 GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC       393
106 Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
107 100                 105                 110                 115
109 CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC       441
110 Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp
111                 120                 125                 130
113 ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC       489
114 Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe
115             135                 140                 145
117 CAC CCA CGC TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC       537
118 His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile
119         150                 155                 160
121 CCA GAA GGG GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC       585
122 Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp
123     165                 170                 175
125 TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT       633
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Input Set : N:\Crf3\RULE60\10083825.raw
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```
126 Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr
127 180                 185                 190                 195
129 CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC       681
130 Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu
131                 200                 205                 210
133 GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC       729
134 Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp
135             215                 220                 225
137 ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG       777
138 Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu
139         230                 235                 240
141 GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC       825
142 Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro
143     245                 250                 255
145 AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC       873
146 Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro
147 260                 265                 270                 275
149 TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC       921
150 Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile
151                 280                 285                 290
153 CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC       969
154 Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro
155             295                 300                 305
157 AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC      1017
158 Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser
159         310                 315                 320
161 AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC      1065
162 Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe
163     325                 330                 335
165 CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC      1113
166 Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala
167 340                 345                 350                 355
169 GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG      1161
170 Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met
171                 360                 365                 370
173 AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC      1209
174 Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn
175             375                 380                 385
177 CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC      1257
178 Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala
179         390                 395                 400
181 ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA      1305
182 Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys
183     405                 410                 415
185 TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC          1351
186 Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
187 420                 425                 430
189 GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG    1411
191 GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG    1471
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PATENT APPLICATION: US/10/083,825 TIME: 14:14:06

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TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC 1531
ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAC 1591
GCATAAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT 1651
CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG 1711
GGCGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC 1771
CTGTAATAAA TGTCACAATA AAACGAATGA ATGAAAAAAA AAAAAAAAAA A 1822

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
1 5 10 15
Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
20 25 30
Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
35 40 45
Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
50 55 60
Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
65 70 75 80
Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
85 90 95
Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
100 105 110
Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
115 120 125
Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
130 135 140
Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
145 150 155 160
Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
165 170 175
Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
180 185 190
Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
195 200 205
Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
210 215 220
Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
225 230 235 240
His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
245 250 255
Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
260 265 270
Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
275 280 285

RAW SEQUENCE LISTING DATE: 05/16/2002
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```
271 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
272     290                 295                 300
274 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
275 305                 310                 315                 320
277 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
278                 325                 330                 335
280 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
281             340                 345                 350
283 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
284         355                 360                 365
286 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
287     370                 375                 380
289 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
290 385                 390                 395                 400
292 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
293                 405                 410                 415
295 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
296             420                 425                 430
299 (2) INFORMATION FOR SEQ ID NO: 3:
301      (i) SEQUENCE CHARACTERISTICS:
302           (A) LENGTH: 102 amino acids
303           (B) TYPE: amino acid
304           (D) TOPOLOGY: linear
306     (ii) MOLECULE TYPE: protein
309     (ix) FEATURE:
310           (A) NAME/KEY: Protein
311           (B) LOCATION: 1..102
312           (D) OTHER INFORMATION: /label= OPX
313 /note= "WHEREIN EACH XAA IS INDEPENDENTLY SELECTED
314 FROM A GROUP OF ONE OR MORE SPECIFIED AMINO ACIDS
315 AS DEFINED IN THE SPECIFICATION"
318     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
W--> 320      Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa
321      1               5                   10                  15
W--> 323      Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
324                  20                  25                  30
W--> 326      Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
327              35                  40                  45
W--> 329      Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
330          50                  55                  60
W--> 332      Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
333      65                  70                  75                  80
W--> 335      Asp Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys Xaa Arg Asn Met Val Val
336                  85                  90                  95
W--> 338      Xaa Ala Cys Gly Cys His
339                  100
```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/16/2002
PATENT APPLICATION: US/10/083,825 TIME: 14:14:07

Input Set : N:\Crf3\RULE60\10083825.raw
Output Set: N:\CRF3\05162002\J083825.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos.2,3,9,11,16,19,23,26,35,39,41,50,52,56,57,58,60,61,65,71,73
Seq#:3; Xaa Pos.75,80,82,84,87,89,91,97

VERIFICATION SUMMARY DATE: 05/16/2002
PATENT APPLICATION: **US/10/083,825** TIME: 14:14:07

Input Set : **N:\Crf3\RULE60\10083825.raw**
Output Set: **N:\CRF3\05162002\J083825.raw**

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:16
L:326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:32
L:329 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:48
L:332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:64
L:335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:80
L:338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:96